SEQUENCE LISTING

SEQ ID NO: 1 is primate GPR2 nucleotide sequence.
SEQ ID NO: 2 is primate GPR2 amino acid sequence.
SEQ ID NO: 3 is rodent GPR2 nucleotide sequence.
SEQ ID NO: 4 is rodent GPR2 amino acid sequence.
SEQ ID NO: 5 is primate Vic nucleotide sequence.
SEQ ID NO: 6 is primate Vic amino acid sequence.
SEQ ID NO: 7 is alternative primate Vic nucleotide sequence.
SEQ ID NO: 8 is alternative primate Vic amino acid sequence.
SEQ ID NO: 9 is rodent Vic nucleotide sequence.
SEQ ID NO: 10 is rodent Vic amino acid sequence.
SEQ ID NO: 11 is primate CTACK nucleotide sequence.
SEQ ID NO: 12 is primate CTACK amino acid sequence.
SEQ ID NO: 13 is rodent CTACK nucleotide sequence.
SEQ ID NO: 14 is rodent CTACK amino acid sequence.
SEQ ID NO: 15 provides a primate actin PCR primer sequence.
SEQ ID NO: 16 provides a primate actin PCR primer sequence.

<110> Wang, Wei
Oldham, Elizabeth R.
Soto, Hortensia
Liu, Ying
Hudak, Susan A.
Homey, Bernhard
Morales, Janine M.
Kellermann, Sirid-Aimee
McEvoy, Leslie M.
Bowman, Edward P.
Zlotnik, Albert

<120> Chemokine and Receptor Uses; Compositions; Methods

<130> DX0882XK

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<160> 16

<170> PatentIn Ver. 2.0

<210> 1
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<212> DNA
<213> primate

<220>
<221> CDS
<222> (1)..(1086)

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Met Gly Thr Glu Val Leu Glu Gln Val Ser Trp Gly His Tyr Ser Gly
  1               5                  10                  15

gat gaa gag gac gca tac tcg gct gag cca ctg ccg gag ctt tgc tac   96
Asp Glu Glu Asp Ala Tyr Ser Ala Glu Pro Leu Pro Glu Leu Cys Tyr
            20                  25                  30

aag gcc gat gtc cag gcc ttc agc cgg gcc ttc caa ccc agt gtc tcc  144
Lys Ala Asp Val Gln Ala Phe Ser Arg Ala Phe Gln Pro Ser Val Ser
        35                  40                  45

ctg acg ctg gct gcg ctg ggt ctg gcc ggc aat ggc ctg gtc ctg gcc  192
Leu Thr Leu Ala Ala Leu Gly Leu Ala Gly Asn Gly Leu Val Leu Ala
    50                  55                  60

acc cac ctg gca gcc cga cgc gca gcg cgc tcg ccc acc tct gcc cac  240
Thr His Leu Ala Ala Arg Arg Ala Ala Arg Ser Pro Thr Ser Ala His
65                  70                  75                  80

ctg ctc cag ctg gcc ctg gcc gac ctc ttg ctg gcc ctg act ctg ccc  288
Leu Leu Gln Leu Ala Leu Ala Asp Leu Leu Leu Ala Leu Thr Leu Pro
                85                  90                  95

ttc gcg gca gca ggg gct ctt cag ggc tgg agt ctg gga agt gcc acc  336
Phe Ala Ala Ala Gly Ala Leu Gln Gly Trp Ser Leu Gly Ser Ala Thr
            100                 105                 110

tgc cgc acc atc tct ggc ctc tac tcg gcc tcc ttc cac gcc ggc ttc  384
Cys Arg Thr Ile Ser Gly Leu Tyr Ser Ala Ser Phe His Ala Gly Phe
        115                 120                 125

ctc ttc ctg gcc tgt atc agc gcc gac cgc tac gtg gcc atc gcg cga  432
Leu Phe Leu Ala Cys Ile Ser Ala Asp Arg Tyr Val Ala Ile Ala Arg
    130                 135                 140

gcg ctc cca gcc ggg ccg cgg ccc tcc act ccc ggc cgc gca cac ttg  480
Ala Leu Pro Ala Gly Pro Arg Pro Ser Thr Pro Gly Arg Ala His Leu
145                 150                 155                 160

gtc tcc gtc atc gtg tgg ctg ctg tca ctg ctc ctg gcg ctg cct gcg  528
Val Ser Val Ile Val Trp Leu Leu Ser Leu Leu Leu Ala Leu Pro Ala
                165                 170                 175

ctg ctc ttc agc cag gat ggg cag cgg gaa ggc caa cga cgc tgt cgc  576
Leu Leu Phe Ser Gln Asp Gly Gln Arg Glu Gly Gln Arg Arg Cys Arg
            180                 185                 190

ctc atc ttc ccc gag ggc ctc acg cag acg gtg aag ggg gcg agc gcc  624
Leu Ile Phe Pro Glu Gly Leu Thr Gln Thr Val Lys Gly Ala Ser Ala
        195                 200                 205

gtg gcg cag gtg gcc ctg ggc ttc gcg ctg ccg ctg ggc gtc atg gta  672
Val Ala Gln Val Ala Leu Gly Phe Ala Leu Pro Leu Gly Val Met Val
    210                 215                 220
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gcc tgc tac gcg ctt ctg ggc cgc acg ctg ctg gcc gcc agg ggg ccc   720
Ala Cys Tyr Ala Leu Leu Gly Arg Thr Leu Leu Ala Ala Arg Gly Pro
225                 230                 235                 240

gag cgc cgg cgt gcg ctg cgc gtc gtg gtg gct ctg gtg gcg gcc ttc   768
Glu Arg Arg Arg Ala Leu Arg Val Val Val Ala Leu Val Ala Ala Phe
                245                 250                 255

gtg gtg ctg cag ctg ccc tac agc ctc gcc ctg ctg ctg gat act gcc   816
Val Val Leu Gln Leu Pro Tyr Ser Leu Ala Leu Leu Leu Asp Thr Ala
            260                 265                 270

gat cta ctg gct gcg cgc gag cgg agc tgc cct gcc agc aaa cgc aag   864
Asp Leu Leu Ala Ala Arg Glu Arg Ser Cys Pro Ala Ser Lys Arg Lys
        275                 280                 285

gat gtc gca ctg ctg gtg acc agc ggc ttg gcc ctc gcc cgc tgt ggc   912
Asp Val Ala Leu Leu Val Thr Ser Gly Leu Ala Leu Ala Arg Cys Gly
    290                 295                 300

ctc aat ccc gtt ctc tac gcc ttc ctg ggc ctg cgc ttc cgc cag gac   960
Leu Asn Pro Val Leu Tyr Ala Phe Leu Gly Leu Arg Phe Arg Gln Asp
305                 310                 315                 320

ctg cgg agg ctg cta cgg ggt ggg agc tcg ccc tca ggg cct caa ccc   1008
Leu Arg Arg Leu Leu Arg Gly Gly Ser Ser Pro Ser Gly Pro Gln Pro
                325                 330                 335

cgc cgc ggc tgc ccc cgc cgg ccc cgc ctt tct tcc tgc tca gct ccc   1056
Arg Arg Gly Cys Pro Arg Arg Pro Arg Leu Ser Ser Cys Ser Ala Pro
            340                 345                 350

acg gag acc cac agt ctc tcc tgg gac aac tag                      1089
Thr Glu Thr His Ser Leu Ser Trp Asp Asn
        355                 360
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<213> primate

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Asp Glu Glu Asp Ala Tyr Ser Ala Glu Pro Leu Pro Glu Leu Cys Tyr
            20                  25                  30

Lys Ala Asp Val Gln Ala Phe Ser Arg Ala Phe Gln Pro Ser Val Ser
        35                  40                  45

Leu Thr Leu Ala Ala Leu Gly Leu Ala Gly Asn Gly Leu Val Leu Ala
    50                  55                  60

Thr His Leu Ala Ala Arg Arg Ala Ala Arg Ser Pro Thr Ser Ala His
65                  70                  75                  80
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Leu Leu Gln Leu Ala Leu Ala Asp Leu Leu Leu Ala Leu Thr Leu Pro
85 90 95

Phe Ala Ala Ala Gly Ala Leu Gln Gly Trp Ser Leu Gly Ser Ala Thr
100 105 110

Cys Arg Thr Ile Ser Gly Leu Tyr Ser Ala Ser Phe His Ala Gly Phe
115 120 125

Leu Phe Leu Ala Cys Ile Ser Ala Asp Arg Tyr Val Ala Ile Ala Arg
130 135 140

Ala Leu Pro Ala Gly Pro Arg Pro Ser Thr Pro Gly Arg Ala His Leu
145 150 155 160

Val Ser Val Ile Val Trp Leu Leu Ser Leu Leu Leu Ala Leu Pro Ala
165 170 175

Leu Leu Phe Ser Gln Asp Gly Gln Arg Glu Gly Gln Arg Arg Cys Arg
180 185 190

Leu Ile Phe Pro Glu Gly Leu Thr Gln Thr Val Lys Gly Ala Ser Ala
195 200 205

Val Ala Gln Val Ala Leu Gly Phe Ala Leu Pro Leu Gly Val Met Val
210 215 220

Ala Cys Tyr Ala Leu Leu Gly Arg Thr Leu Leu Ala Ala Arg Gly Pro
225 230 235 240

Glu Arg Arg Arg Ala Leu Arg Val Val Val Ala Leu Val Ala Ala Phe
245 250 255

Val Val Leu Gln Leu Pro Tyr Ser Leu Ala Leu Leu Leu Asp Thr Ala
260 265 270

Asp Leu Leu Ala Ala Arg Glu Arg Ser Cys Pro Ala Ser Lys Arg Lys
275 280 285

Asp Val Ala Leu Leu Val Thr Ser Gly Leu Ala Leu Ala Arg Cys Gly
290 295 300

Leu Asn Pro Val Leu Tyr Ala Phe Leu Gly Leu Arg Phe Arg Gln Asp
305 310 315 320

Leu Arg Arg Leu Leu Arg Gly Gly Ser Ser Pro Ser Gly Pro Gln Pro
325 330 335

Arg Arg Gly Cys Pro Arg Arg Pro Arg Leu Ser Ser Cys Ser Ala Pro
340 345 350

Thr Glu Thr His Ser Leu Ser Trp Asp Asn
355 360

<210> 3
<211> 1089
<212> DNA
<213> rodent

<220>
<221> CDS
<222> (1)..(1086)

<400> 3

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atg ggg acc aag ccc aca gag cag gtc tcc tgg gga ctt tac tcc ggg   48
Met Gly Thr Lys Pro Thr Glu Gln Val Ser Trp Gly Leu Tyr Ser Gly
  1               5                  10                  15

tac gat gag gag gcc tat tcg gtt ggg ccg ctg cca gag ctc tgt tac   96
Tyr Asp Glu Glu Ala Tyr Ser Val Gly Pro Leu Pro Glu Leu Cys Tyr
             20                  25                  30

aag gct gat gtc cag gct ttc agt cgg gcc ttc caa ccc agt gtc tcc   144
Lys Ala Asp Val Gln Ala Phe Ser Arg Ala Phe Gln Pro Ser Val Ser
         35                  40                  45

ctg atg gtg gct gta ctg ggt ctg gct ggc aat ggc cta gtc ttg gcc   192
Leu Met Val Ala Val Leu Gly Leu Ala Gly Asn Gly Leu Val Leu Ala
     50                  55                  60

acc cat ctg gca gcc aga cga act acc cga tct ccc acc tcc gtt cac   240
Thr His Leu Ala Ala Arg Arg Thr Thr Arg Ser Pro Thr Ser Val His
 65                  70                  75                  80

ctg ctc cag ttg gcc ctg gct gac ctt tta ttg gcc ctg act ttg cct   288
Leu Leu Gln Leu Ala Leu Ala Asp Leu Leu Leu Ala Leu Thr Leu Pro
                 85                  90                  95

ttt gct gca gca ggg gct ctt cag ggc tgg aat cta gga agt acc acc   336
Phe Ala Ala Ala Gly Ala Leu Gln Gly Trp Asn Leu Gly Ser Thr Thr
            100                 105                 110

tgc cgt gcc atc tca ggc ctc tac tcg gcc tct ttc cac gct ggc ttc   384
Cys Arg Ala Ile Ser Gly Leu Tyr Ser Ala Ser Phe His Ala Gly Phe
        115                 120                 125

ctc ttc cta gcc tgt atc agc gcc gac cgc tat gtg gcc atc gca cga   432
Leu Phe Leu Ala Cys Ile Ser Ala Asp Arg Tyr Val Ala Ile Ala Arg
    130                 135                 140

gct ctc cca gcc ggg cag cgg ccc tca acg cct agc cga gcg cac ttg   480
Ala Leu Pro Ala Gly Gln Arg Pro Ser Thr Pro Ser Arg Ala His Leu
145                 150                 155                 160

gtt tca gtc ttc gtg tgg ctg ttg gcg ctg ttt ctg gct cta cct gcg   528
Val Ser Val Phe Val Trp Leu Leu Ala Leu Phe Leu Ala Leu Pro Ala
                165                 170                 175
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ctc ctt ttc agc cgg gac ggg cca cgt gaa ggc caa cga cgc tgt cgg   576
Leu Leu Phe Ser Arg Asp Gly Pro Arg Glu Gly Gln Arg Arg Cys Arg
            180                 185                 190

ctc att ttt ccc gaa agc ctc acg cag act gtg aaa ggg gca agc gca   624
Leu Ile Phe Pro Glu Ser Leu Thr Gln Thr Val Lys Gly Ala Ser Ala
        195                 200                 205

gtg gcg cag gtg gtc ctc ggc ttc gcg ctc cct ctg ggc gtc atg gca   672
Val Ala Gln Val Val Leu Gly Phe Ala Leu Pro Leu Gly Val Met Ala
    210                 215                 220

gcc tgt tat gcg ctc ctg ggc cgc acg ctt ctg gcc gcc agg ggg cca   720
Ala Cys Tyr Ala Leu Leu Gly Arg Thr Leu Leu Ala Ala Arg Gly Pro
225                 230                 235                 240

gag cgg cgg cgt gca ctg cgc gtc gtg gtg gct ttg gtg gtg gcc ttc   768
Glu Arg Arg Arg Ala Leu Arg Val Val Val Ala Leu Val Val Ala Phe
                245                 250                 255

gtg gtg ctg cag ttg ccc tac agc ctt gcc ctg ctg ctg gat aca gcc   816
Val Val Leu Gln Leu Pro Tyr Ser Leu Ala Leu Leu Leu Asp Thr Ala
            260                 265                 270

gat cta ctg gca gcc cgc gag cgg agc tgc tcc tcc agc aag cgc aag   864
Asp Leu Leu Ala Ala Arg Glu Arg Ser Cys Ser Ser Ser Lys Arg Lys
        275                 280                 285

gat cta gct ttg ctg gtc acc ggc ggc ttg acc ctg gtc cgt tgc agc   912
Asp Leu Ala Leu Leu Val Thr Gly Gly Leu Thr Leu Val Arg Cys Ser
    290                 295                 300

ctc aat ccg gtg ctt tat gcc ttt ttg ggc ctg cgt ttc cgc cgg gac   960
Leu Asn Pro Val Leu Tyr Ala Phe Leu Gly Leu Arg Phe Arg Arg Asp
305                 310                 315                 320

ctg cgg agg ctg ctc cag ggc gga gga tgc agc ccg aag ccc aac cct  1008
Leu Arg Arg Leu Leu Gln Gly Gly Gly Cys Ser Pro Lys Pro Asn Pro
                325                 330                 335

cgt ggc cgc tgc ccc cgt cga ctc cgc ctt tct tcc tgc tct gct cct  1056
Arg Gly Arg Cys Pro Arg Arg Leu Arg Leu Ser Ser Cys Ser Ala Pro
            340                 345                 350

act gag acc cac agt ctc tct tgg gac aac tag                     1089
Thr Glu Thr His Ser Leu Ser Trp Asp Asn
        355                 360
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<200> 4
<211> 362
<212> PRT
<213> rodent

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            20                  25                  30

Lys Ala Asp Val Gln Ala Phe Ser Arg Ala Phe Gln Pro Ser Val Ser
        35                  40                  45

Leu Met Val Ala Val Leu Gly Leu Ala Gly Asn Gly Leu Val Leu Ala
    50                  55                  60

Thr His Leu Ala Ala Arg Arg Thr Thr Arg Ser Pro Thr Ser Val His
65                  70                  75                  80

Leu Leu Gln Leu Ala Leu Ala Asp Leu Leu Leu Ala Leu Thr Leu Pro
                85                  90                  95

Phe Ala Ala Ala Gly Ala Leu Gln Gly Trp Asn Leu Gly Ser Thr Thr
            100                 105                 110

Cys Arg Ala Ile Ser Gly Leu Tyr Ser Ala Ser Phe His Ala Gly Phe
        115                 120                 125

Leu Phe Leu Ala Cys Ile Ser Ala Asp Arg Tyr Val Ala Ile Ala Arg
    130                 135                 140

Ala Leu Pro Ala Gly Gln Arg Pro Ser Thr Pro Ser Arg Ala His Leu
145                 150                 155                 160

Val Ser Val Phe Val Trp Leu Leu Ala Leu Phe Leu Ala Leu Pro Ala
                165                 170                 175

Leu Leu Phe Ser Arg Asp Gly Pro Arg Glu Gly Gln Arg Arg Cys Arg
            180                 185                 190

Leu Ile Phe Pro Glu Ser Leu Thr Gln Thr Val Lys Gly Ala Ser Ala
        195                 200                 205

Val Ala Gln Val Val Leu Gly Phe Ala Leu Pro Leu Gly Val Met Ala
    210                 215                 220

Ala Cys Tyr Ala Leu Leu Gly Arg Thr Leu Leu Ala Ala Arg Gly Pro
225                 230                 235                 240

Glu Arg Arg Arg Ala Leu Arg Val Val Val Ala Leu Val Val Ala Phe
                245                 250                 255

Val Val Leu Gln Leu Pro Tyr Ser Leu Ala Leu Leu Leu Asp Thr Ala
            260                 265                 270

Asp Leu Leu Ala Ala Arg Glu Arg Ser Cys Ser Ser Ser Lys Arg Lys
        275                 280                 285

Asp Leu Ala Leu Leu Val Thr Gly Gly Leu Thr Leu Val Arg Cys Ser
    290                 295                 300

Leu Asn Pro Val Leu Tyr Ala Phe Leu Gly Leu Arg Phe Arg Arg Asp
305                 310                 315                 320
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Leu Arg Arg Leu Leu Gln Gly Gly Gly Cys Ser Pro Lys Pro Asn Pro
325 330 335

Arg Gly Arg Cys Pro Arg Arg Leu Arg Leu Ser Ser Cys Ser Ala Pro
340 345 350

Thr Glu Thr His Ser Leu Ser Trp Asp Asn
355 360

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<222> (56)..(436)

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<221> mat_peptide
<222> (122)..(436)

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<221> misc_feature
<222> (529)
<223> V; may be A, C, or G

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Met

cag cag aga gga ctc gcc atc gtg gcc ttg gct gtc tgt gcg gcc cta 106
Gln Gln Arg Gly Leu Ala Ile Val Ala Leu Ala Val Cys Ala Ala Leu
-20 -15 -10

cat gcc tca gaa gcc ata ctt ccc att gcc tcc agc tgt tgc acg gag 154
His Ala Ser Glu Ala Ile Leu Pro Ile Ala Ser Ser Cys Cys Thr Glu
-5 -1 1 5 10

gtt tca cat cat att tcc aga agg ctc ctg gaa aga gtg aat atg tgt 202
Val Ser His His Ile Ser Arg Arg Leu Leu Glu Arg Val Asn Met Cys
15 20 25

cgc atc cag aga gct gat ggg gat tgt gac ttg gct gct gtc atc ctt 250
Arg Ile Gln Arg Ala Asp Gly Asp Cys Asp Leu Ala Ala Val Ile Leu
30 35 40

cat gtc aag cgc aga aga atc tgt gtc agc ccg cac aac cat act gtt 298
His Val Lys Arg Arg Arg Ile Cys Val Ser Pro His Asn His Thr Val
45 50 55

aag cag tgg atg aaa gtg caa gct gcc aag aaa aat ggt aaa gga aat 346
Lys Gln Trp Met Lys Val Gln Ala Ala Lys Lys Asn Gly Lys Gly Asn
60 65 70 75

gtt tgc cac agg aag aaa cac cat ggc aag agg aac agt aac agg gca 394
Val Cys His Arg Lys Lys His His Gly Lys Arg Asn Ser Asn Arg Ala
80 85 90

cat cag ggg aaa cac gaa aca tac ggc cat aaa act cct tat 436
His Gln Gly Lys His Glu Thr Tyr Gly His Lys Thr Pro Tyr
95 100 105

tagagagtct acagataaat ctacagagac aattcctcaa gtggacttgg ccatgattgg 496

ttgtcctgca tactgatgaa actactgatg tcvgctggtc tgaaaggacc taccagaagc 556

taaatctcca agaatgccat ttccctatcc ctaatgattc aatctccctt accctgacca 616

atcagtggcc caaattttcc agccccttgc ctcccagaac cccagcccag aactcttcag 676

agatttaaga atctcctcct acctcctgac tcagccccat gtaatcatta aactc 731

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<400> 6
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-5 -1 1 5 10

Glu Val Ser His His Ile Ser Arg Arg Leu Leu Glu Arg Val Asn Met
15 20 25

Cys Arg Ile Gln Arg Ala Asp Gly Asp Cys Asp Leu Ala Ala Val Ile
30 35 40

Leu His Val Lys Arg Arg Arg Ile Cys Val Ser Pro His Asn His Thr
45 50 55

Val Lys Gln Trp Met Lys Val Gln Ala Ala Lys Lys Asn Gly Lys Gly
60 65 70

Asn Val Cys His Arg Lys Lys His His Gly Lys Arg Asn Ser Asn Arg
75 80 85 90

Ala His Gln Gly Lys His Glu Thr Tyr Gly His Lys Thr Pro Tyr
95 100 105

<210> 7
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<213> primate

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<221> CDS
<222> (1)..(492)

<400> 7

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Met Ser Arg Leu Arg Arg Tyr Glu Val Ala Leu Glu Ala Glu Glu Glu
  1               5                  10                  15

atc tac tgg ggc tgc ttc tac ttt ttt cct tgg ctg cga atg tgg cgc   96
Ile Tyr Trp Gly Cys Phe Tyr Phe Phe Pro Trp Leu Arg Met Trp Arg
             20                  25                  30

agg gag cgg agt ccg atg tct cca aca agc cag aga cta agt ctg gaa   144
Arg Glu Arg Ser Pro Met Ser Pro Thr Ser Gln Arg Leu Ser Leu Glu
         35                  40                  45

gcc ccc agc ctc cca ctg aga agc tgg cat ccg tgg aac aag act aag   192
Ala Pro Ser Leu Pro Leu Arg Ser Trp His Pro Trp Asn Lys Thr Lys
     50                  55                  60

cag aag caa gaa gcc ttg cct ctg ccc tcc agc act agc tgc tgt act   240
Gln Lys Gln Glu Ala Leu Pro Leu Pro Ser Ser Thr Ser Cys Cys Thr
 65                  70                  75                  80

cag ctc tat aga cag cca ctc cca agc agg ctg ctg agg agg att gtc   288
Gln Leu Tyr Arg Gln Pro Leu Pro Ser Arg Leu Leu Arg Arg Ile Val
                 85                  90                  95

cac atg gaa ctg cag gag gcc gat ggg gac tgt cac ctc cag gct gtc   336
His Met Glu Leu Gln Glu Ala Asp Gly Asp Cys His Leu Gln Ala Val
            100                 105                 110

gtg ctt cac ctg gct cgg cgc agt gtc tgt gtt cat ccc cag aac cgc   384
Val Leu His Leu Ala Arg Arg Ser Val Cys Val His Pro Gln Asn Arg
        115                 120                 125

agc ctg gct cgg tgg tta gaa cgc caa ggg aaa agg ctc caa ggg act   432
Ser Leu Ala Arg Trp Leu Glu Arg Gln Gly Lys Arg Leu Gln Gly Thr
    130                 135                 140

gta ccc agt tta aat ctg gta cta caa aag aaa atg tac tca aac ccc   480
Val Pro Ser Leu Asn Leu Val Leu Gln Lys Lys Met Tyr Ser Asn Pro
145                 150                 155                 160

caa cag caa aac taataaagca acattagacg acaaaaaaaa aaaaaaaaaa       532
Gln Gln Gln Asn

aaaaaaaaaa a                                                      543
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<210> 8
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<213> primate

<400> 8

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Met Ser Arg Leu Arg Arg Tyr Glu Val Ala Leu Glu Ala Glu Glu Glu
  1               5                  10                  15

Ile Tyr Trp Gly Cys Phe Tyr Phe Phe Pro Trp Leu Arg Met Trp Arg
             20                  25                  30
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Arg Glu Arg Ser Pro Met Ser Pro Thr Ser Gln Arg Leu Ser Leu Glu
35 40 45

Ala Pro Ser Leu Pro Leu Arg Ser Trp His Pro Trp Asn Lys Thr Lys
50 55 60

Gln Lys Gln Glu Ala Leu Pro Leu Pro Ser Ser Thr Ser Cys Cys Thr
65 70 75 80

Gln Leu Tyr Arg Gln Pro Leu Pro Ser Arg Leu Leu Arg Arg Ile Val
85 90 95

His Met Glu Leu Gln Glu Ala Asp Gly Asp Cys His Leu Gln Ala Val
100 105 110

Val Leu His Leu Ala Arg Arg Ser Val Cys Val His Pro Gln Asn Arg
115 120 125

Ser Leu Ala Arg Trp Leu Glu Arg Gln Gly Lys Arg Leu Gln Gly Thr
130 135 140

Val Pro Ser Leu Asn Leu Val Leu Gln Lys Lys Met Tyr Ser Asn Pro
145 150 155 160

Gln Gln Gln Asn

<210> 9
<211> 393
<212> DNA
<213> rodent

<220>
<221> CDS
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<220>
<221> mat_peptide
<222> (67)..(390)

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Met Gln Gln Ala Gly Leu Thr Leu Met Ala Val Ala Val Cys Val Ala
-20 -15 -10

ttt caa acc tca gaa gcc ata ctt ccc atg gcc tcc agc tgt tgc act 96
Phe Gln Thr Ser Glu Ala Ile Leu Pro Met Ala Ser Ser Cys Cys Thr
-5 -1 1 5 10

gag gtg tct cat cat gtt tcc gga aga ctt ctg gaa aga gtg agt tca 144
Glu Val Ser His His Val Ser Gly Arg Leu Leu Glu Arg Val Ser Ser
15 20 25

tgc agc atc cag aga gct gac ggg gac tgc gac ctg gct gct gtc atc 192
Cys Ser Ile Gln Arg Ala Asp Gly Asp Cys Asp Leu Ala Ala Val Ile
30 35 40

```
ctt cat gtt aaa cgt aga aga atc tgc atc agc ccg cac aat cgt act   240
Leu His Val Lys Arg Arg Arg Ile Cys Ile Ser Pro His Asn Arg Thr
         45                  50                  55

ttg aag cag tgg atg aga gcc tca gag gta aag aag aat ggc aga gaa   288
Leu Lys Gln Trp Met Arg Ala Ser Glu Val Lys Lys Asn Gly Arg Glu
     60                  65                  70

aac gtc tgt tct ggg aaa aaa caa ccc agc agg aag gac aga aaa ggg   336
Asn Val Cys Ser Gly Lys Lys Gln Pro Ser Arg Lys Asp Arg Lys Gly
 75                  80                  85                  90

cac act acg aga aag cac aga aca cgt gga aca cac agg cac gaa gcc   384
His Thr Thr Arg Lys His Arg Thr Arg Gly Thr His Arg His Glu Ala
                 95                 100                 105

tct cgt tag                                                      393
Ser Arg
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<210> 10
<211> 130
<212> PRT
<213> rodent

<400> 10

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Met Gln Gln Ala Gly Leu Thr Leu Met Ala Val Ala Val Cys Val Ala
        -20                 -15                 -10

Phe Gln Thr Ser Glu Ala Ile Leu Pro Met Ala Ser Ser Cys Cys Thr
     -5                  -1   1                   5                  10

Glu Val Ser His His Val Ser Gly Arg Leu Leu Glu Arg Val Ser Ser
                 15                  20                  25

Cys Ser Ile Gln Arg Ala Asp Gly Asp Cys Asp Leu Ala Ala Val Ile
             30                  35                  40

Leu His Val Lys Arg Arg Arg Ile Cys Ile Ser Pro His Asn Arg Thr
         45                  50                  55

Leu Lys Gln Trp Met Arg Ala Ser Glu Val Lys Lys Asn Gly Arg Glu
     60                  65                  70

Asn Val Cys Ser Gly Lys Lys Gln Pro Ser Arg Lys Asp Arg Lys Gly
 75                  80                  85                  90

His Thr Thr Arg Lys His Arg Thr Arg Gly Thr His Arg His Glu Ala
                 95                 100                 105

Ser Arg
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<210> 11
<211> 362
<212> DNA

<213> primate

<220>
<221> CDS
<222> (1)..(336)

<220>
<221> mat_peptide
<222> (73)..(336)

<400> 11

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atg aag ggg ccc cca acc ttc tgc agc ctc ctg ctg ctg tca ttg ctc   48
Met Lys Gly Pro Pro Thr Phe Cys Ser Leu Leu Leu Leu Ser Leu Leu
                -20                 -15                 -10

ctg agc cca gac cct aca gca gca ttc cta ctg cca ccc agc act gcc   96
Leu Ser Pro Asp Pro Thr Ala Ala Phe Leu Leu Pro Pro Ser Thr Ala
            -5                  -1   1                  5

tgc tgt act cag ctc tac cga aag cca ctc tca gac aag cta ctg agg   144
Cys Cys Thr Gln Leu Tyr Arg Lys Pro Leu Ser Asp Lys Leu Leu Arg
     10                  15                  20

aag gtc atc cag gtg gaa ctg cag gag gct gac ggg gac tgt cac ctc   192
Lys Val Ile Gln Val Glu Leu Gln Glu Ala Asp Gly Asp Cys His Leu
 25                  30                  35                  40

cag gct ttc gtg ctt cac ctg gct caa cgc agc atc tgc atc cac ccc   240
Gln Ala Phe Val Leu His Leu Ala Gln Arg Ser Ile Cys Ile His Pro
                45                  50                  55

cag aac ccc agc ctg tca cag tgg ttt gag cac caa gag aga aag ctc   288
Gln Asn Pro Ser Leu Ser Gln Trp Phe Glu His Gln Glu Arg Lys Leu
            60                  65                  70

cat ggg act ctg ccc aag ctg aat ttt ggg atg cta agg aaa atg ggc   336
His Gly Thr Leu Pro Lys Leu Asn Phe Gly Met Leu Arg Lys Met Gly
        75                  80                  85

tgaagcccca atagccaaat aataaa                                     362
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<400> 12

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Met Lys Gly Pro Pro Thr Phe Cys Ser Leu Leu Leu Leu Ser Leu Leu
                -20                 -15                 -10

Leu Ser Pro Asp Pro Thr Ala Ala Phe Leu Leu Pro Pro Ser Thr Ala
            -5                  -1   1                  5

Cys Cys Thr Gln Leu Tyr Arg Lys Pro Leu Ser Asp Lys Leu Leu Arg
     10                  15                  20

Lys Val Ile Gln Val Glu Leu Gln Glu Ala Asp Gly Asp Cys His Leu
 25                  30                  35                  40
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Gln Ala Phe Val Leu His Leu Ala Gln Arg Ser Ile Cys Ile His Pro
                  45                  50                  55

Gln Asn Pro Ser Leu Ser Gln Trp Phe Glu His Gln Glu Arg Lys Leu
              60                  65                  70

His Gly Thr Leu Pro Lys Leu Asn Phe Gly Met Leu Arg Lys Met Gly
          75                  80                  85

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                        Met Met Glu Gly Leu Ser Pro Ala Ser Ser
                        -25                 -20

ctc ccg ctg tta ctg ttg ctt ctg agc ccg gct cct gaa gca gcc ttg  100
Leu Pro Leu Leu Leu Leu Leu Leu Ser Pro Ala Pro Glu Ala Ala Leu
-15                 -10                 -5                  -1   1

cct ctg ccc tcc agc act agc tgc tgt act cag ctc tat aga cag cca  148
Pro Leu Pro Ser Ser Thr Ser Cys Cys Thr Gln Leu Tyr Arg Gln Pro
                5                   10                  15

ctc cca agc agg ctg ctg agg agg att gtc cac atg gaa ctg cag gag  196
Leu Pro Ser Arg Leu Leu Arg Arg Ile Val His Met Glu Leu Gln Glu
          20                  25                  30

gcc gat ggg gac tgt cac ctc cag gct gtc gtg ctt cac ctg gct cgg  244
Ala Asp Gly Asp Cys His Leu Gln Ala Val Val Leu His Leu Ala Arg
     35                  40                  45

cgc agt gtc tgt gtt cat ccc cag aac cgc agc ctg gct cgg tgg tta  292
Arg Ser Val Cys Val His Pro Gln Asn Arg Ser Leu Ala Arg Trp Leu
 50                  55                  60                  65

gaa cgc caa ggg aaa agg ctc caa ggg act gta ccc agt tta aat ctg  340
Glu Arg Gln Gly Lys Arg Leu Gln Gly Thr Val Pro Ser Leu Asn Leu
                70                  75                  80

gta cta caa aag aaa atg tac tca aac ccc caa cag caa aac          382
Val Leu Gln Lys Lys Met Tyr Ser Asn Pro Gln Gln Gln Asn
            85                  90                  95

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<400> 14

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Leu	Leu	Ser	Pro	Ala	Pro	Glu	Ala	Ala	Leu	Pro	Leu	Pro	Ser	Ser	Thr
				-5				-1	1				5		

Ser	Cys	Cys	Thr	Gln	Leu	Tyr	Arg	Gln	Pro	Leu	Pro	Ser	Arg	Leu	Leu
		10					15					20			

Arg	Arg	Ile	Val	His	Met	Glu	Leu	Gln	Glu	Ala	Asp	Gly	Asp	Cys	His
	25					30					35				

Leu	Gln	Ala	Val	Val	Leu	His	Leu	Ala	Arg	Arg	Ser	Val	Cys	Val	His
40					45					50					55

Pro	Gln	Asn	Arg	Ser	Leu	Ala	Arg	Trp	Leu	Glu	Arg	Gln	Gly	Lys	Arg
				60					65					70	

Leu	Gln	Gly	Thr	Val	Pro	Ser	Leu	Asn	Leu	Val	Leu	Gln	Lys	Lys	Met
			75					80					85		

Tyr	Ser	Asn	Pro	Gln	Gln	Gln	Asn
			90				95

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<210> 16
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<400> 16
CGTCATACTC CTGCTTGCTG ATCCACATCT GC 32